

Date: Jun 7, 2001 12:10 AM
 OM of: US-09-494-297-2 to: Pending_Patents_NA_Main: *
 About: Results were produced by the Gencore software, version 4.5,
 Copyright (c) 1993-2000 Compugen Ltd.
 Command line parameters:
 -MODEL=frame+, p2n, model -DEV=x1P
 -O=/cgnl_1/ruspro_spool/US09494297/runat_06062001_115736_12362/app_query.fasta_1.825
 -DB=Pending_Patents_NA_Main -OFMT=fastaP -TRIM=rpmp
 -GAP0=12.000 -GAPEXT=4.000 -MINMATCH=1.00 -LOOPEXT=0.000
 -LOOPEXT=0.000 -QGAP0=4.500 -QGAPEXT=0.050 -XGAP0=10.000
 -XGAPEXT=0.500 -FGAP0=6.000 -DEL0=7.000 -DFGAP0=7.000 -YGAP0=10.000
 -YGAPEXT=5.000 -DELEX0=6.000 -DFGAPEXT=7.000 -START=1
 -MATRIX=blosum62 -TRANS=human40.cdt -LIST=45 -DCALIGN=200
 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -NODE=LOCAL
 -OUTTYPE=PFS -NORM=EXT -MINLEN=0 -MAXLEN=2000000000
 -USER=US09494297_@CGNL_1_7660 -NCPD=6 -ICPU=3 -LONGLOG -NO_XLPPY
 -WAIT -THRSHDS=1

246 LeuSerIlePheGluUserGluAspLysGlyAspLysAspTyrRisGlyPhGlyAspM 538
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 2241 TCTTGGCTTCCCCAACTACAACTAAAGGAAAGCTTCAT.T 2284
 ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 262 YrglnAsnLeuLeuSerGlyGlyLeuValProThrLysProProThrPro 278
 ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 2285 ATCACAACACCGTGAATTAGCA...GTCCTGGTACAGTCAGAAAA 2331
 ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 279 GlyAspProProMetProProAsnGlnInProGlnInThrSerVal. 293
 ||||:||||:||||:||||:||||:||||:||||:||||:
 2332 ATCAGGATACATCTGGAAACACAGAGCGTCAAGCCATTAGATT 2381
 ||||:||||:||||:||||:||||:||||:
 294 LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuIleGlu 309
 ||||:||||:||||:||||:||||:||||:||||:
 2382 AAAAGTATCATAAAATCTCTCAGTGAG.AAAACCTACTGG 2425
 ||||:||||:||||:||||:||||:||||:
 309 IyalThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArg 325
 ||||:||||:||||:||||:||||:||||:
 2467 TTAGTGGACAAATAAGTGAGTGGTAATAATGT.CAAACHACA 2466
 ::||||:||||:||||:||||:
 326 ValProSerSerAsnAsp.IleGlyGluArgIleGlu 338
 ::||||:||||:||||:
 247 TTAGTGGACAAATAAGTGAGTGGTAATAATGT.CAAACHACA 2516
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 338 uSerAspGly...ThrThrIleLeuThrGluLeuAsnSerProAlaGlyT 354
 ::||||:||||:||||:
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 ::||||:||||:||||:
 354 YrSerIleAlaGluProLeuThrPheLysValGluAla.Gly 367
 ::||||:||||:||||:
 2567 ATGAGTAGGCAGAAACGACTTGGCAAATGGGAGCAGGAGCAAGC 2616
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 368 LysValIleThrIleLeuAspGlyLysGlnIleGluAsnProAsnLysG 384
 ::||||:||||:||||:
 2617 AAAGT.AGCATGATGAGCAAGAAGGACCAACATCAGT 2660
 ::||||:||||:
 384 uLeuValGluProTyrSerValGluAlaIleAsnAspPheGluGlyPhe 401
 ::||||:||||:
 2661 TATT.CCATGGAAATGAA.AAATAATTTCCTCTTG 2698
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 401 erVal.LeuThrIleLeu.AspTyr 408
 ::||||:||||:
 2699 CAAATAGAAATTAGAAATACACCATGCAAATGCAACAACTGAACTA 2748
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 409 AlalysPheTyrTyrAla.LysAsnLysAsnGlySerSerG 422
 ::||||:||||:
 2749 GCGAGGAGCAGTTGGTTGAAAGAAAATGCTAACAGGAGTTACCA 2798
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 422 nValValTyrCysPheAsnAlaAspLeuLysSerProAspSerGluA 439
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 439 SPGLYGLYLYSThrMetThrProAspPheThrThrGlyGluValLysTyr 455
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 456 ThrHistIleAlaGlyArgAspLeuPheLysThrValLysProArgA 472
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 2832 2832
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 472 pThrAspProAspThrPheLeuLysHistIleLysValleGluLysG 489
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 2833TGGCTTACATGAACTGGACCTG 2860
 ::||||:||||:
 489 LY...TyrArgGluLysGlyGlyInAlaIleGlyTyrSerGlyIleThrGlu 504
 ::||||:||||:
 2861 GTGAGTAAACGCA.ATGGTGAACATCAGGA. 2889
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 505 ThrglnIeuaGalaAlaIleGlnLeuAlaIleTyrTyrPheThrAspSe 521
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 506 ||||:||||:||||:||||:||||:||||:||||:||||:||||:
 NUMBER OF SEQUENCES: 982
 CORRESPONDENCE ADDRESS:

seq_name: /cgn1_7/ptodata/1/pnay/us090_COMB.seq.US-09-070-927-45
 seq_documentation_block:
 ; Sequence 45, Application US/09070927
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Kunsch
 ; APPLICANT: Patrick J. Dillon
 ; APPLICANT: Steven C. Barash
 ; TIME OF INVENTION: Enterococcus faecalis Polynucleotides and
 ; TITLE OF INVENTION: Polypeptides
 ; NUMBER OF SEQUENCES: 982
 ; CORRESPONDENCE ADDRESS:

521 rAlaGluLeuAspLysAspLysLeuLysAspTyrRisGlyPhGlyAspM 538
 ||||:||||:||||:||||:||||:||||:||||:||||:
 2932GTTGATAA. 2949
 ; TATGGAAA.
 538 etasnAspSerThrLeuAlaValAlaLysIleLeuValGluThrAlaGln 554
 ; :||||:||||:
 2950ATTCACTATGCGGC 2964
 ; :||||:||||:
 555AspSerAsnProProGlnLeuThrAspLeuAspPhePheI 568
 ; :||||:||||:
 2965 AAAATATTTGAGAAATGCCGAGAATGGCA. 2997
 ; :||||:||||:
 568 eProAsnAsnAsnLysLysTyrGlnSerLeuIleGlyLysThrGlnThrBisProG 585
 ; :||||:||||:
 2997 2997
 ; :||||:||||:
 585 luasPleuValAspIleIleArgMetGluAspLysGluVallePro 601
 ; :||||:||||:
 2998 CTGACACATCCAAATAATTTGAAACCTTTGACTTAACAGTCATAASAA 3047
 ; :||||:||||:
 602 ValThrHisAsnIleThrLeuAlaGlyS.ThValThrGlyLe 615
 ; :||||:||||:
 3048 AGCCGATAATCAGACG. 3076
 ; :||||:||||:
 632 sLysGlnIleLeuSerGlnInThrValLysThrAspLysThrAsnIe 648
 ; :||||:||||:
 3077 CGAAATTCCGTTAACAGGA.CCAGATACGGATAT 3111
 ; :||||:||||:
 649 GluDhe.LysAspGlyLysAlaThr.IleAsnIle 659
 ; :||||:||||:
 3112 GAATTACCAAAGATGGCAAGAACGGGATACTTTGTTTGAAACT 3161
 ; :||||:||||:
 659 uLysHisGlyGlu.SerIleThrLeuGlyLeuProGlyLysT 675
 ; :||||:||||:
 3162 AAACACCAGGGAAATATGTTCTACAGAAACCTTACGCCGAAAGGATTC 3211
 ; :||||:||||:
 675 erTyrIleLeuValLysGluThrAsp.SerGluLysTyroLysI 688
 ; :||||:||||:
 3212 AGGGGTTAAAGAACCACTGCAATTAATATTCTGAGAATGGTCAGTC 3261
 ; :||||:||||:
 689 LysValAsnSerGlnGluValAlaAsnAlaThrValSer.Ly 702
 ; :||||:||||:
 3262 AGCATAGATGGAAAGACTAGCAGATGTTTAATTCGGAGAGAA 3311
 ; :||||:||||:
 702 sThrGlyIleThrSerAspGluLeuAlaIlePheGluAsnAsnLysGlu 719
 ; :||||:||||:
 3312 TAATCAAAATTTACTTTAGACCTTACG.AACCGCAAAAGGTC 3352
 ; :||||:||||:
 719 rovalValProThrGlyValAspGlnLysIleAsnGlyTyrLeuAla 735
 ; :||||:||||:
 3353 CTTTACCTGAAACCTGGCATAGGACGCTTGCGTTTACTCTGATAGCG 3402
 ; :||||:||||:
 736 Ile.ValleAlaGlyIleSerLeuGlyLys 745
 ; :||||:||||:
 3403 ATTAGTACATTCGIGATAGCGGGCTTACTCTCTTATT 3441
 ; :||||:||||:

ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 6/33
 OPERATING SYSTEM: MS DOS version 6.2
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/070,927
 FILING DATE: herewith
 CLASSIFICATION:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: A. Anders Brookes
 REGISTRATION NUMBER: 36,373
 REFERENCE/DOCKET NUMBER: PB369

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15614 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 ; US-09-070-927-45

alignment_scores:
 alignment block: US-09-494-297-2 x US-09-070-927-45

Align seg 1/1 to: US-09-070-927-45 from: 1 to: 15614

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 110 nLeuLysLysAlaPheLeuGlySerAspSerSerValLysThrPT 127
 |||:||| ::|||:||| ::|||:||| 9112TGGGTAAGGCCAGAGATTCAATTCATT 9142
 127 YRLysLysHISAspGlyIleSerThrLysPheGluAsp..... 139
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 140TyRAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLys 154
 |||:||| ::|||:||| ::|||:||| 9187 TTTGGPATCAATGATGGTGGACAACTTCAGCCATTGGCCAGGC 9236
 154 SIEuAGaLavalMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleM 171
 ::|||:||| ::|||:||| ::|||:||| 9237 CCCTGAaaaAGCTGATT.....GGGTTG 9262
 171 etGluGlyLeuGluProLeuAsnAlaIleArgValThrGlnGluAlaVal 187
 |||:||| ::|||:||| ::|||:||| 9263 CTTCGGGAAAGCACC.....GGCGTGAGTTAACGTAAAAATC 9306
 188 TPTyPTyTyrSerAspAsnAlaProLeuSerAsnProAspGluSerPhyL 204
 |||:||| ::|||:||| ::|||:||| 9307 TGGGAAGAGTAGATGATCAGACCCGACAACTGGCCAGATAATGTGATTA 9356
 204 SARGGIUserGluUserAsnLeuValSerThrSer..... 215

9357 TGAATTTAGTAGAAGCAAGTACTGACACGCCAACTGGCAACTGGGT 9406
 216GlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuLeuLysPro 230
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 231 AsnLeuAlaThrLysMetProLysGlnValProAspAspPheGln..... 245
 ::|||:||| ::|||:||| ::|||:||| 9457 AAAATGTAACCCAACTTCCAAACCGCAGTGAAGCTAACTCAGAGT 9506
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 262 YRGlnAsnLeuLeuSerGlyGlyLeuValProThrLysProProThrPro 278
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 294 ...LeuIleArgLysIleSerGlyAspLysSerIleLeuLysLeuLys 309
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 309 LYAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArg 325
 |||:||| ::|||:||| ::|||:||| 9692 GACCCGCTTGTGATGTTGGTAAATGTT.....CARACACA 9732
 326 ValPheserSerAsnAsp.....IleGlyGluArgIleGluIle 338
 ::|||:||| ::|||:||| ::|||:||| 9733 TTAGTGACAAATAAGATGTTAGTATTCCTGCCCCAAAGATGTCGCT 9782
 338 uSerAspAspIly...ThrTyrIleIleGluLeuAsnSerProAlaIgyl 354
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 354 YF-SerTleAlaGluProLeuThrPheLysValGluAla.....Gly 367
 ::|||:||| ::|||:||| ::|||:||| 9833 ATGAGTTAGGCAAGAACGCTTGGCAATTTGGTAGCTGAGCAGG 9882
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 401 erVal.....LeuThrThrGlnAsnTyRAlaLysPheTyrTyr 413
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 430 SpleuLysSerProProAspSerGluLysGlyIlySthMetThrPro 446
 10043 10057
 447 AspPheThrThrGlyGluValLysTyrThrIleAlaGlyIargAspLe 463
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10112 AAATTAGGAACTGGTGTAGTATCGA..... 10138
 496 AlalegclutyrsergylLeuthrGluthrLneurargAlaAlanthrgl 512
 10139 ATGGTGGACATCAGGA..... CCATTAGCTACGACACTCT 10176
 512 nleuAlaLleLtyrTyPheThrAspSerAlaGluLeuAspLysAspLys 529
 10177 TGCTGGAAATATGAAATTCT..... GTTGATCAA..... 10207
 529 eulysAspTyR-HisGlyPheGlyAspMetAsnAspSerThrLeuAlaVal 545
 10208 TATGGAA..... 10216
 546 AlalysIleLeuValGluTyPAlaGin..... AspSerAspProP 559
 10217 ATTCACATATGCAGGCCAAATAATTGAGAAATGCGCC 10254
 559 ognLLeuThrAspPheHeleProAsnAsnAsnLysTyrglnS 576
 10225 AGAAATGACA..... 10264
 576 erLeuIleGlyThrGlnTrpHisProGluAspLeuValAspIleIearg 592
 10264 10264
 593 MetGluLysAspLysGluValLeProValThrHisAsnLeuThrLeuAr 609
 10265 CTGACACATCAAATAATTGAA 10287
 609 gLys..... ThrValTrgLyIleAlaGlyAspArgThrLysAspP 623
 10288 ACCTTTTGACTAACAGTAA..... 10330
 623 heHisPheGluIleGluLeuLysAsnLysGlnGluLeuLeuSerGln 639
 10331 CCACTTAAGGGCGAAATCCGTTAACAGGA..... 10363
 640 ThrValLySthrAspLysThrAsnLeuGluPhe... LysAspGlyLysAl 655
 10364 CCAGATACGGATATTGAA..... 10401
 655 aThr..... IleAsnIleuLysHisGlyGlu... SerLeuT 666
 10402 AACGGATRACTTTGTTTGTGAAACTTAACCAAGGGAAATATGTTCTAA 10451
 666 hrLeuIglnGlyLeuPcoglLgLyTySerrIleLeuValIysGluThrAsp 682
 10452 CAGAAACCTTTACGCCAGAAGGATAACAGGGTTAAAGAACCCATCGAA 10501
 683 SerGluGlyTyRlysValLysValAsnSerGlnGluValAl 696
 10502 TTAATAATTCGTGAGATGGTCAGTCACCGTAGATGGGAAAGTAGC 10551
 696 aAsnAlaThrValSer..... LysThrGlyIleThrSerAspPGLut 710
 10552 AGATGTTTTAAATTCTCAGAGAGAACTTAACAAATTACTTTAGACGTTA 10601
 710 hrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyValAsp 726
 10602 CG..... ACCAGCAAAAGTTCTTACCTGAAACGUGGTGCA 10642
 727 GlntysrIleasnGlyTyRlysValLeuAlaLeuIle..... ValIleAlaG 740
 10643 GGACGCTTGIGCTTACTGATAGGGATAGTACATCGTGATAGGG 10692
 740 yIleSerLreLgLyIle 745
 10693 TGTAACTCTCTTTATT 10708
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 seq_documentation_block:

Sequence 45, Application US/09070927A
 GENERAL INFORMATION:
 APPLICANT: Charles A. Kunsch
 Patrick J. Dillon
 Steven Barash
 TITLE OF INVENTION: *faecalis* Polynucleotides and Polypeptides
 NUMBER OF SEQUENCES: 982
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MS DOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/070,927A
 FILING DATE: 04-May-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/046,655
 FILING DATE: 1997-05-16
 APPLICATION NUMBER: 60/044,031
 FILING DATE: 1997-05-06
 APPLICATION NUMBER: 60/066,009
 FILING DATE: 1997-11-14
 ATTORNEY/AGENT INFORMATION:
 NAME: Kenley K. Hover
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 REFERENCE/DOCKET NUMBER: PB369
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 LENGTH: 15614 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 ;
 SEQUENCE DESCRIPTION: SEQ ID NO: 45:
 US-09-070-927A-45

alignment_scores:
 Quality: 196.00 Length: 706
 Ratio: 0.596 Gaps: 42
 Percent Similarity: 46.601 Percent Identity: 22.946
 alignment_block:
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 Align seg 1/1 to: US-09-070-927A-45 from: 1 to: 15614
 96 ValAsnLeuGluGlySer..... ArgSerTyrglnValTyrcySpheAs 110
 9070 GNGTCGCTAACAGGCCTACATTAGTATAGTATGATTAT..... 9111
 110 nleuLysLysAlaPheProLeuGlySerAspSerSerValLysLysTrp 127
 9112 TTGGGTAAAGGCAAAATCAATTCAATTCAATTCAATTCAATT 9142
 127 YLysLysHisAspGlyIleSerThrLysPheGluAsp..... 139
 9143 ATCAAGTACGT..... ATTCACAGAGTCAGAAACTTCACACCTGAT 9186
 140 TyraAlaMetSerProArgIleThgLyAspGluLeuAsnGlnLys 154
 9187 TTGTGCTATCAATGATGGGACACGTTTCAGCCATTAGGCACGGC 9236

10602 CG.....AACCAAGGAAAGGTCTTACCTGAACCTGGTGCATA 10642
 727 GlnLysIleasnGlytyrLeuAlaLeuL... ValLeAlaG1 740
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: 139
 10643 GAGACCTTGTTGTTTACTGATAGCGATAGTACATTCGATAGCGG 10692
 740 YIleSerLeuGlyIle 745
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: 111
 10693 TGTATPATCTTATT 10708
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 seq_documentation_block:
 sequence 1048, application US/60045649
 GENERAL INFORMATION:
 APPLICANT: Lagace, Robert E.
 APPLICANT: Corely, Neil C.
 APPLICANT: Russo, Frank D.
 APPLICANT: Hahn, Amy L.
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAECALIS
 NUMBER OF SEQUENCES: 1466
 NUMBER OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 TELECOMMUNICATION INFORMATION:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/60/045,649
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: CERONE, MICHAEL C.
 REGISTRATION NUMBER: 39,132
 REFERENCE/DOCKET NUMBER: PM-0003P
 TELEPHONE: (415) 855-0555
 TELEFAX: (415) 845-4166
 INFORMATION FOR SEQ ID NO: 1048:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7971 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 IMMEDIATE SOURCE:
 CLONE: EF01048
 US-60-045-649-1048
 alignment_scores:
 alignment_block:
 US-09-494-297-2 x US-60-045-649-1048 ..
 Align seg 1/1 to: US-60-045-649-1048 from: 1 to: 7971
 96 ValLeuLeuGlyIleSer... ArgSerTyrGlnValTyrCysPheAsn 110
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: 111
 1672 GTGTCGCTAACGGCCTACATTAATAGTATGAGTATGAT... 1713
 110 nLeuLysIleAlaProLeuGlySerAspSerSerValLysTrpT 127
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: 111
 127 YrLysLysHsAspGlyIleSerThrLysPheGluAsp... 139
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: 111
 1745 ATCAAGTACCT.....ATCAGAACAGACTCAGAACACTGAT 1788
 140TyAlaMetSerProArgIleThrGlyAspGluLeuasnGly 154
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: 111
 1789 TTTGGTATCACTGAACTGGTGGACAAAGCTTCGCGATTACCCACGC 1838
 154 sLeuArgAlaValMettryAsnGlyHisProGlnAsnAlaAsnGly 154
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 1839 CCCGAAAGATGTTT.....GGGGTC 1864
 188 TrpTyrTyrSerAspAsnalaProIleSerAsnProAspGlu... 204
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: 111
 1909 TGGAAGAGTATGATCAAGACCCACAAGCTGGCAGATAATGATTA 1958
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: 111
 1865 CTTGGGAAAGACCT.....GGCGTGAAGTTAACGTTAAAC 1908
 204 ysATGluSerGluSerAsnLeuValser.....ThsSerGlnLeu... 218
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: 111
 1959 TGAATTTAGTAGAAGCAGTACTGACAGACGCCAACTGGT 2008
 ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: 111
 219 LeuMetArgGlnAlaLeuIysGlnLeuIleAsp... 229
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 230ProAsnLeuAlaThrLysMetProLysGlnValProAspA 243
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 293 al.....LeuIleGlyLysTyrAlaLeuGlyAspTyrSerLysIle 306
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 2244 TAGATTTAAAGTAACTCAAATCTTCTCAGGTGA... 3AAGAC 2287
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 2288 TTAGTGGGAGCCGTTTGTGATTGAGTGGTAAATGTT... 2328
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 323 nAlaArgValPheserSerAsnAsp... 336
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 336 IeGluLeuSerAspGly... ThryIleLeuIleGluLeuAsnSerPhe 351
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 2379 TGCGCCATAAAAGGGAGACCTATACTTAATGAGTAATAGCCT 2428
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 323 nlysgluIleValGlyProTyrSerValGluIalysAsnAspPhe... 398
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307 LeuGluGlyAlaThrIleGlnLeuThrGlyAspAsnValAsnSerPheGln 323
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 323 nalaArgValPheSerSerAsnAsp.....IleGlyGluArgI 336
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 336 leGluLeuSerAspGly .. .ThrTrpThrLeuGluLeuAsnSerPro 351
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 407 AsnTyrrAlaLysPheTyrrTyrrAla.....LysAsnLysAsnGlyS 420
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 ; GENERAL INFORMATION:
 ; APPLICANT: Corbin, David R.
 ; APPLICANT: Malvar, Thomas M.
 ; APPLICANT: Shukla, Hridayabhanjan
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS CHROMOSOMAL GENOME SEQUENCES AND
 ; FILE REFERENCE: 38-21(51376)B
 ; CURRENT APPLICATION NUMBER: US/09/663,779
 ; CURRENT FILING DATE: 2000-09-15
 ; PRIORITY APPLICATION NUMBER: 60/154,678
 ; PRIORITY FILING DATE: 1999-09-17
 ; NUMBER OF SEQ ID NOS: 8283
 ; SEQ ID NO 1301
 ; LENGTH: 10627
 ; TYPE: DNA
 ; ORGANISM: Bacillus thuringiensis
 ; US-09-663-779-1301
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 Ratio: 0.612 Gaps: 32
 Percent Similarity: 49.349 Percent Identity: 21.498
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STRANDEDNESS: double
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 MOLECULE TYPE: genomic DNA
 IMMEDIATE SOURCE:
 CLONE: EFM15748
 US-60-068-186-748

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align-seq 1/1 to: US-60-068-186-748 from: 1 to: 18768

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82 s_ProTyRtYRlysGlnPheArgValAlaHisAspLeuArgValAsnLeu 98

12506 CTCCA.....TCTATTCATCA 12522

99 GluGlySer.....ArgSerTyrGlnValTyrCysPheAsnLeuLysLys 113

12523 GAGGAATACTACATCAAGAGCAATCAGATCAT. . 12555

113 sHapheProleuGlySerAspSerValLysLysTyrTyrLysLysH 130

12556 TTTAGGAAAGGCCAAAGAACTCAAATCATTACCAAGTGA 12595

130 isAspGlyLysSerThrLysPheGluAspTyr. . 140

12596 GA.....ATCCAAACGAAATGAGGACTTCCATCCAATTCCTGAT 12639

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12640 CAATGAGCAGCAGCAACTTCCAGCCAAACATGATCACATGAATT 12689

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201 u.....SerPhylsArgGluSerGluSerAsnLeuValSerThrSerGlnL 217

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12830 CTGCAGCTGGAAAGGAAATATCGAACATTAACCGCTAAAGAT 12879

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12930 CGGAGAAAGTATCAGAGAGATTACACTCTAACATAATCAAG 12979

255 LysAspLysTyrAsnLysGlyIrglnAsnLeuLeuSerGlyIrglyLeuAl 271

12980 CTCAGCACTTGT.....TACCAACAACT 13005

272 ProThyRProProThyRProGly.....ASPProPr 282

13006 . . AAAGAAATACCTGACCGAGATACGATTCACAAATAGATGCAAT 13052

282 oMetProProAsnGlnProGlnThrThrSerVal. . 13146

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313 GinLeuThrGlyAspAsnValAsnSerPhGlnAla. . ArgValPhe 328

328 rSerAsnAspIleGlyGluArgIleGluLeu. . SerAspGlyLyrTyrT 344

13197 AACCTATTCCTTCCAGAAATGTCATAATGCAAAAGAAATGACCTATA 13196

344 hrLeuThrGluLeuAsnSerProAlaGlyTyrSerIleAlaGluProIle 360

13247 CGCTGACAGAACAAAGCUCAGAGGCATGATGATGAAAGACT 13296

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13297 ACTTGGAAATCAAGATCGCTCTGATGGTACGGTACCCATTGATGAAA 13346

376 S. . 382

382 slySGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGlu 398

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13558 GATTCACTCACACTCTGGTAAATATCGGAGTGTGIGACACGCTGGTCTGC 13607

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13663 ATCATT. . TACACGGGAAATAACCGAGATGACAAATATGATGAC 13709

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13760 AAGAGAC. . 13788

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 ; Sequence 744, Application US/60050444
 ; GENERAL INFORMATION:
 ; APPLICANT: APPLICANT:Lagace, Robert E.
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Russo, Frank D.
 ; APPLICANT: Hann, Amy L.
 ; APPLICANT: Heath, Joe D.
 ; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FARCALIS
 ; NUMBER OF SEQUENCES: 1063
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:

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 Quality: 180.00 Length: 741
 Ratio: 0.547 Gaps: 41
 Percent Similarity: 44.399 Percent Identity: 20.783

alignment_block:
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413 yr.....AlaLys.....AsnIysAsnGly 419
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 16531 GATGAGCATAGTTGTGACCGCAGTCAGTCAAGATGATATACACA 16580
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 16604 CTTATGATTCACAGATGATGACGCAGATGGCGATGACGATTCAGATGAT 16653
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 16836 ATTAAGATGAGGAGGGTGTATCCGCTTGTGATAC.....AAATAATG 16879

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 634 IuargilegluIeuserAspGlyThrThrLeutIgluIeAspSer 350
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 7096 GAAATGAACTAGCTAGCTCAAGCAGCAAAATATTAACTAAATAA 7145
 408 ralalysPheTyryrValalysAsnlysAsnGlySerGlnValWalt 425
 7146 AGCTGAAACAATAATATAAGACAAACAACTGGACAATATGAA 7195
 410 GIVGlyIVySthMetrrPheTrPheThrIgluIleGly 454
 7246 CATGGTGGATACAATTAAAGATAAGAACTA.. GAAATTAAGCGG 7292
 455 ...TyrThrHisIleIleIgargIargAspIlePhelysTyrThrValIySP 470
 7293 AAATTAAACCCITCAAGCTGACT 7245
 470 roArgAspThrAspProAspThrPheIleIySValIle 486
 7321 TATGTTAGATGACA 7338
 487 GluIVySlyTyArgGlyIgylgIinAlaIleGlyIrrSerGlyIeuth 503
 7339 GATAAACGCTTCAAATTACTCTTATAGGTACGTATCAGTCATAAGAC 7388
 503 rgluthGlnIleIuargAlaAlaIthrGlnIleLeuAlaIleItyrTyPheThra 520
 7389 AAAGACA..... TTTGATTTACAAACCTGAAACTCTCAATT 7417
 520 SPSerAlaIgluLeuAlaIleIysAspIleIys..... AspTyr 532
 7418 AC..... TTGATTTACAAACCTGAAACTCTCAATT 7458
 533 HisGlyPheGlyIaspIteAsn..... AspSerIleLeuIala 545
 7459 AAAATACAGGTAACCTCTGGATGATACGGATCTAACACATC 7508
 545 IalalysIleIeuaIgluIyAlaGlnAspSerAsnProGlnIleut 562
 7509 AAATAAGTTGAGCTATTCGATCTGAT..... 7542
 562 hrAspIleuAspPheIleProAsnAsnIysTyrGlnSer..... 576
 7543 TTCAAGGCAATGTTATAATACGGCTCTATAAC 7581
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7582 GCCAACGGAAGGAATTACTTGATATAGGCTTACTATAATAGT 7631
 585 uASpleu..... ValAspIleIleArgMetGluAspIysL 597
 7632 TGAGATTAAGATGCTTATGTTATAGGCTCA..... CAGATAAAC 7675
 597 ysGluIleProValThrHisAsnIleThrIleuIgargIlysthrValThr 613
 7676 AAAGTGTAGTGCCT..... GGATCCATTGAGTGGCCGATATGATTTA 7719
 614 GlyLeuIalaglyAspArg..... ThrIVySAS 622
 7720 ATGGAAATCCCTGATAATGCAACACCTGGTAATGCTGTACCACTGAGAA 7769
 622 PheHisPheGluIleGluIleIysAsnIysGlyIleu 636
 7770 ATATGAACTTGAGAACTACAGAGAACATAAAACACCTTAAACAGC 7869
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 7820 ATTCACAACATCATATCATCTACCTTACTATATCTTAAACAGC 7819
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 7870 CTTGATGGTAACCTATCCAGGACCTACACAAACAGGCAAGATTTAA 7919
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 8050 .CAACACCATGCGATGCGCGTGTACAGATGACCCACC..... G 8089
 714 IuSN..... AsnIysGluProValValProThrGlyIval 725
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 8140 GAT 8142

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 seq_documentation_block:
 ; Sequence 368, Application US/60068139
 ; GENERAL INFORMATION:
 ; APPLICANT: LAGACE, ROBERT E.
 ; APPLICANT: CORLEY, NEIL C.
 ; APPLICANT: RUSSO, FRANK D.
 ; APPLICANT: HANN, AMY L.
 ; APPLICANT: HEATH, JOE D.
 ; APPLICANT: FINNEY, GREGORY L.
 ; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATTARRHALIS
 ; TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 471
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 60/068,139
 FILING DATE: HERWIWHT
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: CERRONE, MICHAEL C.
 REGISTRATION NUMBER: 39,132
 REFERENCE/DOCKET NUMBER: PM-0008-2 P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 368:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14346 base pairs
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: genomic DNA
 IMMEDIATE SOURCE:
 CLONE: NCALC368
 US-60-068-139-368

alignment_scores:
 Quality: 169 50 Length: 864
 Ratio: 0.479 Gaps: 42
 Percent Similarity: 40.972 Percent Identity: 19.444

alignment_block:
 US-09-494-297-2 x US-60-068-139-368 ..

Align seg 1/1 to: US-60-068-139-368 from: 1 to: 14346

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 58 CCATCACAGCTGATGACATTACAC.....CACTTATTGATAAATTC 601

23 RLYSARGPheThrVal.....ThrLeuValGlyValLeuLeuMetI 37
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37 lePheAlaLeuValThrSerMetValGlyAlaLysThrValPheGlyLeu 53
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54 ValGluSerSerThrProAspAlaLeuAsnProAspSerSerGly 70
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 687 GGTGCAATTGTCACTT.....GCCAAAAACCCA.....ACCTA 721

70 RARGTPTYRGlyTyGluSerTyrValArg.....GlyHisP 83-
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 722 CATGAATATCACAAAGAACAAACATCAAAACAAACCCAGGGATG 771

83 ROTYR.....TYLYsGlnPheArgValAlaHisAsp 93 ..
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94 LeuArgValAsnLeuIleGlySerArgSerGlyGlnValThrCysPheAs 110
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110 nLeuLysLysAlaPheProLeuGlySerAspSerSerValLysLysTrpT 127
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836

127 yLysLysLysAspGlyIleSerThrLysPheGluAspTyrAlaMetSer 143
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144 ProArgIleThrGlyAspGluLeuAsnGlnLysLeuArgAlaValMetty 160

837 GACACCCAGACGACAGAACGACCGTGCATCTTT 871

160 rRangly..... HisProGlnAsnAlaArgValThrGlnGluAlaValTrp 172
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172 luGlyLeuGluProLeuAsnAlaLeuArgValThrGlnGluAlaValTrp 188
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189 TYTYrSerAspAsnAlapro.....IleSerAsnProAspGly 201
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 201 u..... SerPhlysArgGluSerGlySerAspL 211
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 1007 TAAAGTAGGCACTTAACTTAACTTAACTTAAACAGCTTTAAATAAACACACC 1106

211 euValSerThrSerGlnLeuSerLeu..... 219

1057 TGGTAGTGCAGCACACATTATCTAACAGCTTTAAATAAACACACC 1106

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224 ulySglnLeuLeuAspProAspLeuAlaThrLysSerProLysGlnValP 241
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265 uLeuSerGlyGlyLeu..... 274

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1400 AGAAGGGGGTTATGGTGGTGGCGCGCGTGGAGCTG.....G 1437

324 IaArgValPheSerSerAsnAspIle.....Gly 333

1438 CGGTAATTTTATCCATGCAACGCAACTTGTGGCTTGTGG 1487

334 GluArgIleGluLeuSerAspGlyIleThrThrLeuThrGluLeuAsnSe 350
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350 rProAlaGlyTyrSerIleAlaGluProIleThrPheLysValGluAlaLag 367
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367 lLysValTyrThrIleLeuAspGlyLys.....GlnIleGlu 379
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 403 eurthrIhrGluAsnTyAla. LysPheTyTyr 413
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 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
 ; FILE REFERENCE: GTC-005
 ; CURRENT APPLICATION NUMBER: US/09/134,000A
 ; CURRENT FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 6810
 ; SEQ ID NO 1566
 ; LENGTH: 3702
 ; TYPE: DNA
 ; ORGANISM: Enterococcus faecalis
 ; US-09-134-000-1566
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 1836 AGATGTTTCAGTATTAAGTCTACTACGCCAAATACCAACGAAATCCAA 1885
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 1936 ATCCCGAGTCAGTACGATCCAGTAACTACGAGTGGTGAAGGTTACTCC 1985
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 2362 ATACAGSGGACAGCGAAAGAACACCAATCGAATTAATGAAAGAACATT 2411
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 614 GlyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGluLeu 630
 3274 GGTCAAGT...GATAACACAAAGCAGGGTTATCCAAATTATTCAG 3320
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